

PB

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/763,985

DATE: 09/24/2001

TIME: 15:44:13

Input Set : A:\0020-4817P.ST25.txt

Output Set: N:\CRF3\09242001\I763985.raw

3 <110> APPLICANT: ITOH, Kyogo et al.

5 <120> TITLE OF INVENTION: NOVEL TUMOR ANTIGEN PROTEIN SART-3 AND TUMOR ANTIGEN PEPTIDES THEREOF

7 <130> FILE REFERENCE: 0020-4817P

9 <140> CURRENT APPLICATION NUMBER: 09/763,985

10 <141> CURRENT FILING DATE: 2001-02-28

12 <160> NUMBER OF SEQ ID NOS: 64

14 <170> SOFTWARE: PatentIn version 3.1

16 <210> SEQ ID NO: 1

17 <211> LENGTH: 3798

18 <212> TYPE: DNA

19 <213> ORGANISM: Homo sapiens

21 <220> FEATURE:

22 <221> NAME/KEY: CDS

23 <222> LOCATION: (12)..(2900)

24 <223> OTHER INFORMATION:

27 <400> SEQUENCE: 1

ENTERED

P-5

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32 gct gag tcc aag gct ggg ccc aag gct gac gga gag gag gat gag gtt      98
33 Ala Glu Ser Lys Ala Gly Pro Lys Ala Asp Gly Glu Glu Asp Glu Val
34           15           20           25
36 aag gcg gct agg aca agg aga aag gtg tta tcg cgg gct gtg gcc gct      146
37 Lys Ala Ala Arg Thr Arg Arg Lys Val Leu Ser Arg Ala Val Ala Ala
38 30           35           40           45
40 gcg aca tac aag acc atg ggg cca gcg tgg gat cag cag gag gaa ggc      194
41 Ala Thr Tyr Lys Thr Met Gly Pro Ala Trp Asp Gln Gln Glu Glu Gly
42           50           55           60
44 gtg agc gag agc gat ggg gat gag tac gcc atg gct tcc tcc gcg gag      242
45 Val Ser Glu Ser Asp Gly Asp Glu Tyr Ala Met Ala Ser Ser Ala Glu
46           65           70           75
48 agc tcc ccc ggg gag tac gag tgg gaa tat gac gaa gag gag gag aaa      290
49 Ser Ser Pro Gly Glu Tyr Glu Trp Glu Tyr Asp Glu Glu Glu Lys
50           80           85           90
52 aac cag ctg gag att gag aga ctg gag gag cag ttg tct atc aac gtc      338
53 Asn Gln Leu Glu Ile Glu Arg Leu Glu Glu Gln Leu Ser Ile Asn Val
54           95           100          105
56 tat gac tac aac tgc cat gtg gac ttg atc aga ctg ctc agg ctg gaa      386
57 Tyr Asp Tyr Asn Cys His Val Asp Leu Ile Arg Leu Leu Arg Leu Glu
58 110           115           120           125
60 ggg gag ctt acc aag gtg agg atg gcc cgc cag aag atg agt gaa atc      434
61 Gly Glu Leu Thr Lys Val Arg Met Ala Arg Gln Lys Met Ser Glu Ile
62           130           135           140
64 ttt ccc ttg act gaa gag ctc tgg ctg gag tgg ctg cat gac gag atc      482
65 Phe Pro Leu Thr Glu Glu Leu Trp Leu Glu Trp Leu His Asp Glu Ile
66           145           150           155
68 agc atg gcc cag gat ggc ctg gac aga gag cac gtg tat gac ctc ttt      530

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70			160					165					170				
72	gag	aaa	gcc	gtg	aag	gat	tac	att	tgt	cct	aac	att	tgg	cta	gag	tat	578
73	Glu	Lys	Ala	Val	Lys	Asp	Tyr	Ile	Cys	Pro	Asn	Ile	Trp	Leu	Glu	Tyr	
74		175				180					185						
76	ggc	cag	tac	tca	gtt	ggt	ggg	att	ggt	cag	aaa	ggt	ggc	ctt	gag	aaa	626
77	Gly	Gln	Tyr	Ser	Val	Gly	Gly	Ile	Gly	Gln	Lys	Gly	Gly	Leu	Glu	Lys	
78	190					195					200				205		
80	gtt	cgc	tcc	gtg	ttt	gaa	agg	gct	ctc	tcg	tct	gtt	ggt	tta	cat	atg	674
81	Val	Arg	Ser	Val	Phe	Glu	Arg	Ala	Leu	Ser	Ser	Val	Gly	Leu	His	Met	
82				210						215				220			
84	acc	aaa	gga	ctc	gcc	ctc	tgg	gag	gct	tac	cga	gag	ttt	gaa	agt	gcg	722
85	Thr	Lys	Gly	Leu	Ala	Leu	Trp	Glu	Ala	Tyr	Arg	Glu	Phe	Glu	Ser	Ala	
86			225					230					235				
88	att	gtg	gaa	gct	gct	cgg	ctt	gag	aaa	gtc	cac	agt	ctt	ttc	cgg	cga	770
89	Ile	Val	Glu	Ala	Ala	Arg	Leu	Glu	Lys	Val	His	Ser	Leu	Phe	Arg	Arg	
90			240					245					250				
92	cag	ttg	gcg	atc	cca	ctc	tat	gat	atg	gag	gcc	aca	ttt	gca	gag	tat	818
93	Gln	Leu	Ala	Ile	Pro	Leu	Tyr	Asp	Met	Glu	Ala	Thr	Phe	Ala	Glu	Tyr	
94		255				260					265						
96	gaa	gaa	tgg	tca	gaa	gac	cca	ata	cca	gag	tca	gta	att	cag	aac	tat	866
97	Glu	Glu	Trp	Ser	Glu	Asp	Pro	Ile	Pro	Glu	Ser	Val	Ile	Gln	Asn	Tyr	
98	270				275						280			285			
100	aac	aaa	gca	cta	cag	cag	ctg	gag	aaa	tat	aaa	ccc	tat	gaa	gaa	gca	914
101	Asn	Lys	Ala	Leu	Gln	Gln	Leu	Glu	Lys	Tyr	Lys	Pro	Tyr	Glu	Glu	Ala	
102				290						295				300			
104	ctg	ttg	cag	gca	gag	gca	cca	agg	ctg	gca	gaa	tat	caa	gca	tat	atc	962
105	Leu	Leu	Gln	Ala	Glu	Ala	Pro	Arg	Leu	Ala	Glu	Tyr	Gln	Ala	Tyr	Ile	
106			305					310					315				
108	gat	ttt	gag	atg	aaa	att	ggc	gat	cct	gct	cgc	att	cag	ttg	atc	ttt	1010
109	Asp	Phe	Glu	Met	Lys	Ile	Gly	Asp	Pro	Ala	Arg	Ile	Gln	Leu	Ile	Phe	
110		320					325				330						
112	gag	cgc	gcc	ctg	gtc	gag	aac	tgc	ctt	gtc	cca	gac	tta	tgg	atc	cgt	1058
113	Glu	Arg	Ala	Leu	Val	Glu	Asn	Cys	Leu	Val	Pro	Asp	Leu	Trp	Ile	Arg	
114		335				340					345						
116	tac	agt	cag	tac	cta	gat	cga	caa	ctg	aaa	gta	aag	gat	ttg	gtt	tta	1106
117	Tyr	Ser	Gln	Tyr	Leu	Asp	Arg	Gln	Leu	Lys	Val	Lys	Asp	Leu	Val	Leu	
118	350				355					360				365			
120	tct	gta	cat	aac	cgc	gct	att	aga	aac	tgc	ccc	tgg	aca	gtt	gcc	tta	1154
121	Ser	Val	His	Asn	Arg	Ala	Ile	Arg	Asn	Cys	Pro	Trp	Thr	Val	Ala	Leu	
122				370						375				380			
124	tgg	agt	cgg	tac	ctc	ttg	gcc	atg	gag	aga	cat	gga	gtt	gat	cat	caa	1202
125	Trp	Ser	Arg	Tyr	Leu	Leu	Ala	Met	Glu	Arg	His	Gly	Val	Asp	His	Gln	
126			385					390				395					
128	gta	att	tct	gta	acc	ttc	gag	aaa	gct	ttg	aat	gcc	ggc	ttc	atc	cag	1250
129	Val	Ile	Ser	Val	Thr	Phe	Glu	Lys	Ala	Leu	Asn	Ala	Gly	Phe	Ile	Gln	
130		400					405					410					
132	gcc	act	gat	tat	gtg	gag	att	tgg	cag	gca	tac	ctt	gat	tac	ctg	agg	1298
133	Ala	Thr	Asp	Tyr	Val	Glu	Ile	Trp	Gln	Ala	Tyr	Leu	Asp	Tyr	Leu	Arg	

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136 aga agg gtt gat ttc aaa caa gac tcc agt aaa gag ctg gag gag ttg      1346
137 Arg Arg Val Asp Phe Lys Gln Asp Ser Ser Lys Glu Leu Glu Glu Leu
138 430      435      440      445
140 agg gcc gcc ttt act cgt gcc ttg gag tat ctg aag cag gag gtg gaa      1394
141 Arg Ala Ala Phe Thr Arg Ala Leu Glu Tyr Leu Lys Gln Glu Val Glu
142      450      455      460
144 gag cgt ttc aat gag agt ggt gat cca agc tgc gtg att atg cag aac      1442
145 Glu Arg Phe Asn Glu Ser Gly Asp Pro Ser Cys Val Ile Met Gln Asn
146      465      470      475
148 tgg gct agg att gag gct cga ctg tgc aat aac atg cag aaa gct cgg      1490
149 Trp Ala Arg Ile Glu Ala Arg Leu Cys Asn Asn Met Gln Lys Ala Arg
150      480      485      490
152 gaa ctc tgg gat agc atc atg acc aga gga aat gcc aag tac gcc aac      1538
153 Glu Leu Trp Asp Ser Ile Met Thr Arg Gly Asn Ala Lys Tyr Ala Asn
154      495      500      505
156 atg tgg cta gag tat tac aac ctg gaa aga gct cat ggt gac acc cag      1586
157 Met Trp Leu Glu Tyr Tyr Asn Leu Glu Arg Ala His Gly Asp Thr Gln
158 510      515      520      525
160 cac tgc cgg aag gct ctg cac cgg gcc gtc cag tgc acc agt gac tac      1634
161 His Cys Arg Lys Ala Leu His Arg Ala Val Gln Cys Thr Ser Asp Tyr
162      530      535      540
164 cca gag cac gtc tgc gaa gtg tta ctc acc atg gag agg aca gaa ggt      1682
165 Pro Glu His Val Cys Glu Val Leu Leu Thr Met Glu Arg Thr Glu Gly
166      545      550      555
168 tct tta gaa gat tgg gat ata gct gtt cag aaa act gaa acc cga tta      1730
169 Ser Leu Glu Asp Trp Asp Ile Ala Val Gln Lys Thr Glu Thr Arg Leu
170      560      565      570
172 gct cgt gtc aat gag cag aga atg aag gct gca gag aag gaa gca gcc      1778
173 Ala Arg Val Asn Glu Gln Arg Met Lys Ala Ala Glu Lys Glu Ala Ala
174      575      580      585
176 ctt gtg cag caa gaa gaa gaa aag gct gaa caa cgg aaa aga gct cgg      1826
177 Leu Val Gln Gln Glu Glu Glu Lys Ala Glu Gln Arg Lys Arg Ala Arg
178 590      595      600      605
180 gct gag aag aaa gcg tta aaa aag aag aaa aag atc aga ggc cca gag      1874
181 Ala Glu Lys Lys Ala Leu Lys Lys Lys Lys Lys Ile Arg Gly Pro Glu
182      610      615      620
184 aag cgc gga gca gat gag gac gat gag aaa gag tgg ggc gat gat gaa      1922
185 Lys Arg Gly Ala Asp Glu Asp Asp Glu Lys Glu Trp Gly Asp Asp Glu
186      625      630      635
188 gaa gag cag cct tcc aaa cgc aga agg gtc gag aac agc atc cct gca      1970
189 Glu Glu Gln Pro Ser Lys Arg Arg Arg Val Glu Asn Ser Ile Pro Ala
190      640      645      650
192 gct gga gaa aca caa aat gta gaa gta gca gca ggg ccc gct ggg aaa      2018
193 Ala Gly Glu Thr Gln Asn Val Glu Val Ala Ala Gly Pro Ala Gly Lys
194      655      660      665
196 tgt gct gcc gta gat gtg gag ccc cct tcg aag cag aag gag aag gca      2066
197 Cys Ala Ala Val Asp Val Glu Pro Pro Ser Lys Gln Lys Glu Lys Ala
198 670      675      680      685

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204	gac	agc	atc	acc	gtc	ttt	gtc	agc	aac	ctg	ccc	tac	agc	atg	cag	gag	2162
205	Asp	Ser	Ile	Thr	Val	Phe	Val	Ser	Asn	Leu	Pro	Tyr	Ser	Met	Gln	Glu	
206				705					710							715	
208	ccg	gac	acg	aag	ctc	agg	cca	ctc	ttc	gag	gcc	tgt	ggg	gag	gtg	gtc	2210
209	Pro	Asp	Thr	Lys	Leu	Arg	Pro	Leu	Phe	Glu	Ala	Cys	Gly	Glu	Val	Val	
210				720					725							730	
212	cag	atc	cga	ccc	atc	ttc	agc	aac	cgt	ggg	gat	ttc	cga	ggg	tac	tgc	2258
213	Gln	Ile	Arg	Pro	Ile	Phe	Ser	Asn	Arg	Gly	Asp	Phe	Arg	Gly	Tyr	Cys	
214				735				740								745	
216	tac	gtg	gag	ttt	aaa	gaa	gag	aaa	tca	gcc	ctt	cag	gca	ctg	gag	atg	2306
217	Tyr	Val	Glu	Phe	Lys	Glu	Glu	Lys	Ser	Ala	Leu	Gln	Ala	Leu	Glu	Met	
218	750					755				760						765	
220	gac	cgg	aaa	agt	gta	gaa	ggg	agg	cca	atg	ttt	gtt	tcc	ccc	tgt	gtg	2354
221	Asp	Arg	Lys	Ser	Val	Glu	Gly	Arg	Pro	Met	Phe	Val	Ser	Pro	Cys	Val	
222						770				775						780	
224	gat	aag	agc	aaa	aac	ccc	gat	ttt	aag	gtg	ttc	agg	tac	agc	act	tcc	2402
225	Asp	Lys	Ser	Lys	Asn	Pro	Asp	Phe	Lys	Val	Phe	Arg	Tyr	Ser	Thr	Ser	
226						785				790						795	
228	cta	gag	aaa	cac	aag	ctg	ttc	atc	tca	ggc	ctg	cct	ttc	tcc	tgt	act	2450
229	Leu	Glu	Lys	His	Lys	Leu	Phe	Ile	Ser	Gly	Leu	Pro	Phe	Ser	Cys	Thr	
230				800					805							810	
232	aaa	gag	gaa	cta	gaa	gaa	atc	tgt	aag	gct	cat	ggc	acc	gtg	aag	gac	2498
233	Lys	Glu	Glu	Leu	Glu	Glu	Ile	Cys	Lys	Ala	His	Gly	Thr	Val	Lys	Asp	
234				815					820							825	
236	ctc	agg	ctg	gtc	acc	aac	cgg	gct	ggc	aaa	cca	aag	ggc	ctg	gcc	tac	2546
237	Leu	Arg	Leu	Val	Thr	Asn	Arg	Ala	Gly	Lys	Pro	Lys	Gly	Leu	Ala	Tyr	
238	830					835				840						845	
240	gtg	gag	tat	gaa	aat	gaa	tcc	cag	gcg	tcg	cag	gct	gtg	atg	aag	atg	2594
241	Val	Glu	Tyr	Glu	Asn	Glu	Ser	Gln	Ala	Ser	Gln	Ala	Val	Met	Lys	Met	
242						850				855						860	
244	gac	ggc	atg	act	atc	aaa	gag	aac	atc	atc	aaa	gtg	gca	atc	agc	aac	2642
245	Asp	Gly	Met	Thr	Ile	Lys	Glu	Asn	Ile	Ile	Lys	Val	Ala	Ile	Ser	Asn	
246						865				870						875	
248	cct	cct	cag	agg	aaa	gtt	cca	gag	aag	cca	gag	acc	agg	aag	gca	cca	2690
249	Pro	Pro	Gln	Arg	Lys	Val	Pro	Glu	Lys	Pro	Glu	Thr	Arg	Lys	Ala	Pro	
250						880				885						890	
252	ggt	ggc	ccc	atg	ctt	ttg	ccg	cag	aca	tac	gga	gcg	agg	ggg	aag	gga	2738
253	Gly	Gly	Pro	Met	Leu	Leu	Pro	Gln	Thr	Tyr	Gly	Ala	Arg	Gly	Lys	Gly	
254						895				900						905	
256	agg	acg	cag	ctg	tct	cta	ctg	cct	cgt	gcc	ctg	cag	cgc	cca	agt	gct	2786
257	Arg	Thr	Gln	Leu	Ser	Leu	Leu	Pro	Arg	Ala	Leu	Gln	Arg	Pro	Ser	Ala	
258	910					915				920						925	
260	gca	gct	cct	cag	gct	gag	aac	ggc	cct	gcc	gcg	gct	cct	gca	gtt	gcc	2834
261	Ala	Ala	Pro	Gln	Ala	Glu	Asn	Gly	Pro	Ala	Ala	Ala	Pro	Ala	Val	Ala	
262						930				935						940	
264	gcc	cca	gca	gcc	acc	gag	gca	ccc	aag	atg	tcc	aat	gcc	gat	ttt	gcc	2882

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269 Lys Leu Phe Leu Arg Lys
270          960
272 ttactttcact ctggcccggc ggacctccca ccaccagca gtgcactggg gatggacagg      2990
274 cctgggtgtgc tgcgtgctcg caaccacaga tggctcctcg gctttagaca gaaaggggaa      3050
276 ggggtttctaa gtcaagagcc tttcagtgtc ccctcatatt gagggcagtg gcagaaaagt      3110
278 gaccactctg caggctgggc ccaggatgtg gtgtcctgag atagttttgt atcttaaaga      3170
280 ctgaggcaca gaagcgaaac gagaacacac tgtttttgag acacagttgt ccaaattgtt      3230
282 ctggccagct ccggcccctt tttgtatgac acttctcttc caccctgcac agcacatgtg      3290
284 cccgtcattc ttttaatttt aaaagatgaa atggcagatg ctagtaattc acagaatggc      3350
286 ctcttggtggg ggtgggtctg aggggaagtca gctataaaac atttgctgga gttttgttca      3410
288 atgggggctgt gcatttttat attatgtgtt tgtaaattgac atgtcagccc ttgtttcatg      3470
290 tttcctaaaa gcagaatatt tgcaacattt gttttgtata ggaattattt gtgccacctg      3530
292 ctgtggactg ttttctttgc ctagtgacta gtgacctgtg ttgtctaaac atgagtttca      3590
294 gcccttttgt tttgtttaat accatgtcaa atgcaaactt caattctccc catttagctt      3650
296 tattaaactg acgttctctt caaaacttct tgctgaatgg tactcagatg tgcattcaca      3710
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304 <211> LENGTH: 963
305 <212> TYPE: PRT
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315          20          25          30
318 Arg Thr Arg Arg Lys Val Leu Ser Arg Ala Val Ala Ala Ala Thr Tyr
319          35          40          45
322 Lys Thr Met Gly Pro Ala Trp Asp Gln Gln Glu Glu Gly Val Ser Glu
323          50          55          60
326 Ser Asp Gly Asp Glu Tyr Ala Met Ala Ser Ser Ala Glu Ser Ser Pro
327 65          70          75          80
330 Gly Glu Tyr Glu Trp Glu Tyr Asp Glu Glu Glu Glu Lys Asn Gln Leu
331          85          90          95
334 Glu Ile Glu Arg Leu Glu Glu Gln Leu Ser Ile Asn Val Tyr Asp Tyr
335          100          105          110
338 Asn Cys His Val Asp Leu Ile Arg Leu Leu Arg Leu Glu Gly Glu Leu
339          115          120          125
342 Thr Lys Val Arg Met Ala Arg Gln Lys Met Ser Glu Ile Phe Pro Leu
343          130          135          140
346 Thr Glu Glu Leu Trp Leu Glu Trp Leu His Asp Glu Ile Ser Met Ala
347 145          150          155          160
350 Gln Asp Gly Leu Asp Arg Glu His Val Tyr Asp Leu Phe Glu Lys Ala
351          165          170          175
354 Val Lys Asp Tyr Ile Cys Pro Asn Ile Trp Leu Glu Tyr Gly Gln Tyr
355          180          185          190

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Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa. 9/24/01

VERIFICATION SUMMARY

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L:1152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:1178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55
L:1204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
L:1230 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
L:1256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
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L:1360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
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L:1412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64